SEQUENCE LISTING

<110>  Strittmatter, Stephen

<120>  Modulators and Modulation of the Interaction Between RGM and
       Neogenin

<130>  23380-602NATL

<140>  10/519,132
<141>  2003-06-23

<150>  PCT/US03/20147
<151>  2003-06-26

<150>  60/392,062
<151>  2002-06-26

<160>  2

<170>  PatentIn version 3.2

<210>  1
<211>  1445
<212>  PRT
<213>  Homo sapiens

<400>  1

Met Ala Ala Glu Arg Glu Ala Gly Arg Leu Leu Cys Thr Ser Ser Ser
1               5                   10                  15


Arg Arg Cys Cys Pro Pro Pro Leu Leu Leu Leu Leu Pro Leu Leu
            20              25                  30


Leu Leu Leu Gly Arg Pro Ala Ser Gly Ala Ala Ala Thr Lys Ser Gly
        35              40                  45


Ser Pro Pro Gln Ser Ala Gly Ala Ser Val Arg Thr Phe Thr Pro Phe
    50              55                  60


Tyr Phe Leu Val Glu Pro Val Asp Thr Leu Ser Val Arg Gly Ser Ser
65                  70                  75                  80


Val Ile Leu Asn Cys Ser Ala Tyr Ser Glu Pro Ser Pro Asn Ile Glu
                85                  90                  95


Trp Lys Lys Asp Gly Thr Phe Leu Asn Leu Glu Ser Asp Asp Arg Arg
                100                 105                 110

1

```
Gln Leu Leu Pro Asp Gly Ser Leu Phe Ile Ser Asn Val Val His Ser
        115                 120                 125

Lys His Asn Lys Pro Asp Glu Gly Phe Tyr Gln Cys Val Ala Thr Val
        130                 135                 140

Asp Asn Leu Gly Thr Ile Val Ser Arg Thr Ala Lys Leu Thr Val Ala
145                 150                 155                 160

Gly Leu Pro Arg Phe Thr Ser Gln Pro Glu Pro Ser Ser Val Tyr Val
                165                 170                 175

Gly Asn Ser Ala Ile Leu Asn Cys Glu Val Asn Ala Asp Leu Val Pro
                180                 185                 190

Phe Val Arg Trp Glu Gln Asn Arg Gln Pro Leu Leu Leu Asp Asp Arg
                195                 200                 205

Ile Val Lys Leu Pro Ser Gly Thr Leu Val Ile Ser Asn Ala Thr Glu
        210                 215                 220

Gly Asp Gly Gly Leu Tyr Arg Cys Ile Val Glu Ser Gly Gly Pro Pro
225                 230                 235                 240

Lys Phe Ser Asp Glu Ala Glu Leu Lys Val Leu Gln Asp Arg Glu Glu
                245                 250                 255

Ile Val Asp Leu Val Phe Leu Met Arg Pro Ser Ser Met Met Lys Val
                260                 265                 270

Thr Gly Gln Arg Ala Val Leu Pro Cys Val Val Ser Gly Leu Pro Ala
        275                 280                 285

Pro Val Val Arg Trp Met Lys Asn Glu Glu Val Leu Asp Thr Glu Ser
        290                 295                 300

Ser Gly Arg Leu Val Leu Leu Ala Gly Gly Gly Leu Glu Ile Ser Asp
305                 310                 315                 320

Val Thr Glu Asp Asp Ala Gly Thr Tyr Phe Cys Ile Ala Asp Asn Gly
                325                 330                 335

Asn Lys Thr Val Glu Ala Gln Ala Glu Leu Thr Val Gln Val Pro Pro
```

2

```
                340                    345                        350


        Gly Phe Leu Lys Gln Pro Ala Asn Ile Tyr Ala His Glu Ser Met Asp
            355                360                365


        Ile Val Phe Glu Cys Glu Val Thr Gly Lys Pro Thr Pro Thr Val Lys
            370                375                380


        Trp Val Lys Asn Gly Asp Val Val Ile Pro Ser Asp Tyr Phe Lys Ile
        385                390                395                400


        Val Lys Glu His Asn Leu Gln Val Leu Gly Leu Val Lys Ser Asp Glu
                        405                410                415


        Gly Phe Tyr Gln Cys Ile Ala Glu Asn Asp Val Gly Asn Ala Gln Ala
                    420                425                430


        Gly Ala Gln Leu Ile Ile Leu Glu His Ala Pro Ala Thr Thr Gly Pro
                    435                440                445


        Leu Pro Ser Ala Pro Arg Asp Val Val Ala Ser Leu Val Ser Thr Arg
            450                455                460


        Phe Ile Lys Leu Thr Trp Arg Thr Pro Ala Ser Asp Pro His Gly Asp
        465                470                475                480


        Asn Leu Thr Tyr Ser Val Phe Tyr Thr Lys Glu Gly Val Asp Arg Glu
                        485                490                495


        Arg Val Glu Asn Thr Ser Gln Pro Gly Glu Met Gln Val Thr Ile Gln
                    500                505                510


        Asn Leu Met Pro Ala Thr Val Tyr Ile Phe Lys Val Met Ala Gln Asn
                    515                520                525


        Lys His Gly Ser Gly Glu Ser Ser Ala Pro Leu Arg Val Glu Thr Gln
                    530                535                540


        Pro Glu Val Gln Leu Pro Gly Pro Ala Pro Asn Ile Arg Ala Tyr Ala
        545                550                555                560


        Thr Ser Pro Thr Ser Ile Thr Val Thr Trp Glu Thr Pro Leu Ser Gly
                        565                570                575


                                        3
```

```
Asn Gly Glu Ile Gln Asn Tyr Lys Leu Tyr Tyr Met Glu Lys Gly Thr
            580             585             590

Asp Lys Glu Gln Asp Ile Asp Val Ser Ser His Ser Tyr Thr Ile Asn
        595             600             605

Gly Leu Lys Lys Tyr Thr Glu Tyr Ser Phe Arg Val Val Ala Tyr Asn
        610             615             620

Lys His Gly Pro Gly Val Ser Thr Gln Asp Val Ala Val Arg Thr Leu
625             630             635             640

Ser Asp Val Pro Ser Ala Ala Pro Gln Asn Leu Ser Leu Glu Val Arg
                645             650             655

Asn Ser Lys Ser Ile Val Ile His Trp Gln Pro Pro Ser Ser Thr Thr
            660             665             670

Gln Asn Gly Gln Ile Thr Gly Tyr Lys Ile Arg Tyr Arg Lys Ala Ser
            675             680             685

Arg Lys Ser Asp Val Thr Glu Thr Leu Val Thr Gly Thr Gln Leu Ser
        690             695             700

Gln Leu Ile Glu Gly Leu Asp Arg Gly Thr Glu Tyr Asn Phe Arg Val
705             710             715             720

Ala Ala Leu Thr Val Asn Gly Thr Gly Pro Ala Thr Asp Trp Leu Ser
            725             730             735

Ala Glu Thr Phe Glu Ser Asp Leu Asp Glu Thr Arg Val Pro Glu Val
            740             745             750

Pro Ser Ser Leu His Val Arg Pro Leu Val Thr Ser Ile Val Val Ser
            755             760             765

Trp Thr Pro Pro Glu Asn Gln Asn Ile Val Val Arg Gly Tyr Ala Ile
        770             775             780

Gly Tyr Gly Ile Gly Ser Pro His Ala Gln Thr Ile Lys Val Asp Tyr
785             790             795             800
```

4

Lys Gln Arg Tyr Tyr Thr Ile Glu Asn Leu Asp Pro Ser Ser His Tyr
            805                 810             815

Val Ile Thr Leu Lys Ala Phe Asn Asn Val Gly Glu Gly Ile Pro Leu
            820                 825             830

Tyr Glu Ser Ala Val Thr Arg Pro His Thr Val Pro Asp Pro Thr Pro
            835                 840             845

Met Met Pro Pro Val Gly Val Gln Ala Ser Ile Leu Ser His Asp Thr
            850                 855             860

Ile Arg Ile Thr Trp Ala Asp Asn Ser Leu Pro Lys His Gln Lys Ile
865                 870                 875             880

Thr Asp Ser Arg Tyr Tyr Thr Val Arg Trp Lys Thr Asn Ile Pro Ala
            885                 890             895

Asn Thr Lys Tyr Lys Asn Ala Asn Ala Thr Thr Leu Ser Tyr Leu Val
            900                 905             910

Thr Gly Leu Lys Pro Asn Thr Leu Tyr Glu Phe Ser Val Met Val Thr
            915                 920             925

Lys Gly Arg Arg Ser Ser Thr Trp Ser Met Thr Ala His Gly Ala Thr
            930                 935             940

Phe Glu Leu Val Pro Thr Ser Pro Pro Lys Asp Val Thr Val Val Ser
945                 950                 955             960

Lys Glu Gly Lys Pro Arg Thr Ile Ile Val Asn Trp Gln Pro Pro Ser
            965                 970             975

Glu Ala Asn Gly Lys Ile Thr Gly Tyr Ile Ile Tyr Tyr Ser Thr Asp
            980                 985             990

Val Asn Ala Glu Ile His Asp Trp Val Ile Glu Pro Val  Val Gly Asn
            995                 1000                1005

Arg Leu  Thr His Gln Ile Gln  Glu Leu Thr Leu Asp  Thr Pro Tyr
    1010                 1015                 1020

5

```
Tyr Phe  Lys Ile Gln Ala Arg  Asn Ser Lys Gly Met  Gly Pro Met
    1025              1030              1035

Ser Glu  Ala Val Gln Phe Arg  Thr Pro Lys Ala Leu  Gly Ser Ala
    1040              1045              1050

Gly Lys  Gly Ser Arg Leu Pro  Asp Leu Gly Ser Asp  Tyr Lys Pro
    1055              1060              1065

Pro Met  Ser Gly Ser Asn Ser  Pro His Gly Ser Pro  Thr Ser Pro
    1070              1075              1080

Leu Asp  Ser Asn Met Leu Leu  Val Ile Ile Val Ser  Val Gly Val
    1085              1090              1095

Ile Thr  Ile Val Val Val Val  Val Ile Ala Val Phe  Cys Thr Arg
    1100              1105              1110

Arg Thr  Thr Ser His Gln Lys  Lys Lys Arg Ala Ala  Cys Lys Ser
    1115              1120              1125

Val Asn  Gly Ser His Lys Tyr  Lys Gly Asn Cys Lys  Asp Val Lys
    1130              1135              1140

Pro Pro  Asp Leu Trp Ile His  His Glu Arg Leu Glu  Leu Lys Pro
    1145              1150              1155

Ile Asp  Lys Ser Pro Asp Pro  Asn Pro Val Met Thr  Asp Thr Pro
    1160              1165              1170

Ile Pro  Arg Asn Ser Gln Asp  Ile Thr Pro Val Asp  Asn Ser Met
    1175              1180              1185

Asp Ser  Asn Ile His Gln Arg  Arg Asn Ser Tyr Arg  Gly His Glu
    1190              1195              1200

Ser Glu  Asp Ser Met Ser Thr  Leu Ala Gly Arg Arg  Gly Met Arg
    1205              1210              1215

Pro Lys  Met Met Met Pro Phe  Asp Ser Gln Pro Pro  Gln Pro Val
    1220              1225              1230

Ile Ser  Ala His Pro Ile His  Ser Leu Asp Asn Pro  His His His
```

6

```
         1235                    1240                    1245


Phe His  Ser Ser Ser Leu Ala  Ser Pro Ala Arg Ser  His Leu Tyr
    1250             1255             1260


His Pro  Ser Ser Pro Trp Pro  Ile Gly Thr Ser Met  Ser Leu Ser
    1265             1270             1275


Asp Arg  Ala Asn Ser Thr Glu  Ser Val Arg Asn Thr  Pro Ser Thr
    1280             1285             1290


Asp Thr  Met Pro Ala Ser Ser  Ser Gln Thr Cys Cys  Thr Asp His
    1295             1300             1305


Gln Asp  Pro Glu Gly Ala Thr  Ser Ser Ser Tyr Leu  Ala Ser Ser
    1310             1315             1320


Gln Glu  Glu Asp Ser Gly Gln  Ser Leu Pro Thr Ala  His Val Arg
    1325             1330             1335


Pro Ser  His Pro Leu Lys Ser  Phe Ala Val Pro Ala  Ile Pro Pro
    1340             1345             1350


Pro Gly  Pro Pro Leu Tyr Asp  Pro Ala Leu Pro Ser  Thr Pro Leu
    1355             1360             1365


Leu Ser  Gln Gln Ala Leu Asn  His His Ile His Ser  Val Lys Thr
    1370             1375             1380


Ala Ser  Ile Gly Thr Leu Gly  Arg Ser Arg Pro Pro  Met Pro Val
    1385             1390             1395


Val Val  Pro Ser Ala Pro Glu  Val Gln Glu Thr Thr  Arg Met Leu
    1400             1405             1410


Glu Asp  Ser Glu Ser Ser Tyr  Glu Pro Asp Glu Leu  Thr Lys Glu
    1415             1420             1425


Met Ala  His Leu Glu Gly Leu  Met Lys Asp Leu Asn  Ala Ile Thr
    1430             1435             1440


Thr Ala
    1445
```

7

<210> 2
<211> 5198
<212> DNA
<213> Homo sapiens

<400> 2
```
gggggccgcg cgggccgggc cgggccgggc tggagccgag ccctgcggcg cagagaccgg    60

ctgaggcgcg ctgagggaag ggcgcgagcg ctccgcggcg ctatcgccgc cgccgccgcc   120

gccactcgtg gggtagagat ggcggcggag cgcgaagccg ggcgactcct ctgcacctcc   180

tcctcccggc gctgctgtcc gccaccgccg ctgctgctgt tgctgccgct gctgctgctg   240

ctcggacgcc cggcgtccgg cgccgcggcc acgaagagcg gctccccgcc gcagtccgca   300

ggagccagtg ttcgaacatt cactccgttt tattttctgg tggagccgat agacaccctc   360

tcagttagag gctcttctgt tatattaaat tgctcggcat attctgagcc ctctccaaac   420

attgaatgga agaaagatgg gactttttta aacttagaat cagatgatcg acgccagcta   480

ctcccagatg gatctttatt catcagcaac gtggtgcatt ccaaacacaa taagcctgac   540

gaaggtttct atcagtgtgt agccactgtg gataatcttg gaaccattgt cagcagaaca   600

gccaagctca cagtagcagg tcttccaaga tttaccagcc aaccagaacc ttcttcagtc   660

tatgttggaa acagtgcaat tctgaattgt gaagttaatg cagatttggt cccatttgtt   720

aggtgggaac agaatcgaca gccccttctt ctagatgaca ggattgtcaa acttccaagt   780

ggaacactgg ttatcagcaa tgctactgaa ggagatgggg gactctaccg ctgcattgtt   840

gaaagtggtg ggccaccaaa gtttagtgac gaagctgaat tgaaagttct tcaagatcgt   900

gaggaaattg tagacttggt atttctgatg cgaccatttt ctatgatgaa agtcactggt   960

cagcgtgcag tgttgccatg tgttgtctca gggcttcctg ctccagtcgt tagatggatg  1020

aaaaacgaag aagtgcttga cacagaaagc tctggcaggt tggtcttgct agcaggaggt  1080

ggcttggaga tcagtgatgt cactgaggat gatgctggga cttatttttg catagctgat  1140

aatggaaata agacagttga agctcaggcg gagcttactg tgcaagtgcc acctggattc  1200

ttgaaacaac ctgctaacat atatgctcac gaatccatgg acattgtatt tgaatgtgaa  1260

gtcactggga agccaactcc aactgtgaag tgggtcaaga atgggggatgt ggttatcccc  1320

agtgattact ttaaaattgt aaaggaacat aatcttcaag ttttgggtct ggtgaaatca  1380

gatgaagggt ctatcaatg cattgctgag aatgatgttg aaatgcaca agctggagcc  1440

cagctgataa tccttgagca tgcaccagcc acaacgggac cactaccttc agctcctcga  1500
```

8

```
gacgtcgtgg cctccctggt ctctactcgc ttcattaaat tgacatggcg tacacctgca    1560

tcagaccctc atggagacaa tctcacctac tctgtgttct acaccaagga aggggttgat    1620

agggagcgtg ttgagaatac cagccagcca ggagagatgc aggtgactat tcaaaacttg    1680

atgccagcaa ctgtgtacat cttcaaagtt atggctcaaa ataagcatgg ctctggagaa    1740

agttcagctc ctcttcgagt agagacacag cctgaggttc agctccctgg cccagcacct    1800

aatatccgtg cttatgcaac gtcacctact tctatcactg tcacctggga aacaccgtta    1860

tctggcaatg gggaaattca aaattacaaa ttgtactaca tggaaaaagg aactgataaa    1920

gaacaggata ttgatgtttc aagtcactcc tacaccatta atggactgaa gaaatacaca    1980

gaatatagtt tccgagtggt ggcctacaat aaacatggtc ctggagtttc tacacaagat    2040

gttgctgttc gaacattatc agatgttccc agtgctgctc ctcagaatct gtccttagaa    2100

gtgagaaatt caaagagtat agtgatccac tggcagcccc cttcctcaac cacacaaaat    2160

gggcagataa ctggctacaa gattcgatat cgaaaggcct cccgaaaaag tgatgtcact    2220

gagaccttgg taactgggac acagctgtct cagctgattg aaggtcttga tcggggggaca    2280

gaatataact tccgagtcgc tgctctcaca gtcaatggta caggtccagc aactgattgg    2340

ctgtctgctg aaacttttga aagcgaccta gatgaaactc gtgttcctga agtgcccagc    2400

tctcttcatg tccgtccgct cgtcactagc attgtagtga gctggactcc tccagagaac    2460

cagaacattg tggtccgagg ttatgccatc ggttacggca ttggcagccc tcatgcccag    2520

accatcaaag tggactataa acaacgttat tacaccattg aaaacttgga tccaagctct    2580

cattacgtga ttaccttgaa agcatttaac aatgttggcg aaggcatccc cctttatgag    2640

agtgctgtga ccagacctca cacagtgcca gatcccactc ccatgatgcc accagtggga    2700

gttcaggctt ccattctgag tcacgacacc ataaggatta cctgggcaga caactccctg    2760

cccaaacacc agaagattac agactcccgc tactacacag tccggtggaa gaccaacatc    2820

ccagcaaaca cgaagtacaa gaatgcaaat gcaacgacgt taagctattt ggttactggt    2880

ttaaagccaa atacgctcta tgagttctct gtgatggtga ccaaaggcag aaggtcaagc    2940

acgtggagta tgacagctca tggcgctacc tttgaattag ttcctacttc tccacctaag    3000

gatgtgacag ttgtgagtaa ggaaggaaaa cctagaacca tcatagtgaa ctggcagcct    3060

ccctctgaag ctaacggcaa gattacaggt tacatcatct attacagcac ggatgtgaat    3120

gcagagatac atgactgggt tattgaacca gttgtgggaa acagactgac tcaccagatt    3180
```

9

```
caagagttaa cacttgatac gccatactac ttcaaaatcc aggcccggaa ctcaaagggc    3240

atggggccca tgtctgaagc tgtacagttc agaacaccta aagccttagg gtcagcagga    3300

aaaggaagcc gactaccaga cctgggatct gactacaaac ctccaatgag tggcagcaac    3360

agccctcacg ggagccccac ctcccctctg gacagcaaca tgctgctggt catcattgtc    3420

tctgttggcg tcatcactat cgtggtggtt gtggtcattg ctgtcttttg tacccggcgc    3480

accacctctc accagaaaaa gaaacgagct gcgtgcaaat cagtgaatgg ctcccataag    3540

tacaagggca attgcaaaga tgtgaagcct ccagacctat ggatccatca cgagagacta    3600

gagttgaagc ctattgacaa gtctccagat cctaaccctg tcatgactga tactccaatc    3660

cctcgaaact ctcaagatat cacaccagtg gacaattcca tggatagcaa tatccatcaa    3720

aggcggaatt catacagagg gcatgagtca gaggacagca tgtctacact ggctggaagg    3780

aggggaatga gaccaaaaat gatgatgccc tttgactctc agccacctca gcctgtgatt    3840

agtgcccatc ccatccattc cctcgataac cctcaccatc atttccactc cagcagcctc    3900

gcttctccag cccgcagtca tctctaccac ccaagcagcc catggcccat tggcacatcc    3960

atgtcccttt cagacagggc caattccaca gaatctgttc gaaataccc cagcacggac    4020

accatgccag cgtcctcgtc tcagacgtgc tgcactgacc atcaggaccc tgagggtgct    4080

actagctcct cttacttggc cagctcccaa gaggaagact caggccagag tcttcccaca    4140

gcccatgtcc gcccttccca ccctctgaag agcttcgctg tgccagcaat cccacccca    4200

ggacctcctc tctatgatcc tgcactgcca agcacaccat tactgtccca gcaagctctg    4260

aaccatcaca ttcactcagt gaaaacagcc tccatcggga cgttaggaag gagccggcct    4320

cctatgccag tggttgttcc gagtgcccct gaagtacagg agaccaccag gattctggaa    4380

gactccgaga gtagctatga accagatgag ctgaccaaag agatggccca cctggaagga    4440

ctaatgaagg acctaaatgc catcacaaca gcctgatgac cttcgcctgg acatgactcc    4500

aagcctgagt ctacaagtct cggaacttaa ccttgaaaac aaggaattgt acagagtacg    4560

agaggacagc acttgagagc aggagccagc aaaccagcca gtgcctccat gtggggttgg    4620

ctccaggcac agccacctgc cttctcctgg tcagcctgga ttacacttgt gtggaggcag    4680

cttcctttg cctgctgaga gcctgcagga ctgggcacta tgggccaaaa ttttgtgtcc    4740

agggaagagg caagaagtac gacctgcctt ttgctttgtg gtcagtggct tgtgtctttg    4800

tgctgcaact gcatcacttt tatggagtgt agacattggc atttatgtac aattttgtgt    4860

cctattttat tttaccttaa aacactatca gaagccaagg gagtctgtga tgttctctca    4920
```

10

```
agcagttgac acttgactgt ggttccagtt acttacggaa agtcatcaac agtgaggttg    4980

tttgacacca ctgacaggca ttggcttgtt gtgggtttca tttttattct taattctgag    5040

acattgcatc ctctgccagc tgttaatcca tcactttgag gggaggacat gttgcattgc    5100

tgtttgtaag ctttttttatt attttttttat tataattatt aaaggcctga ctttctcctc    5160

tcaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa                            5198
```